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RAW SEQUENCE LISTING

DATE: 03/22/2002

PATENT APPLICATION: US/10/024,130A

TIME: 14:29:06

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03222002\J024130A.raw

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4 <110> APPLICANT: Stevens, Donna
5      Wang, Michelle
6      Rice, John
7      Lanning, Beth
8      Broadwell, David
9      Glassbrook, Norman
10     Sevala, Veeresh
11     Crawford, John
12     Stewart, Sandy
14 <120> TITLE OF INVENTION: METHODS FOR DETERMINING SQUALENE
15     SYNTHASE ACTIVITY
17 <130> FILE REFERENCE: 2148US
19 <140> CURRENT APPLICATION NUMBER: US 10/024,130A
20 <141> CURRENT FILING DATE: 2001-12-17
22 <160> NUMBER OF SEQ ID NOS: 13
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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27 <211> LENGTH: 1599
28 <212> TYPE: DNA
29 <213> ORGANISM: Arabidopsis thaliana
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34 gcttggggac gatgctgaga tatccggatg acatatatcc gctcctgaag atgaaacgag      180
35 cgattgagaa agcggagaag cagatccctc ctgagccaca ctgggggttc tgctattcga      240
36 tgctccacaa ggtttcccgga agcttttctc tcgttattca gcaactcaac accgagctcc      300
37 gtaacgccgt gtgtgtgttc tacttggttc tccgagctct tgatactgtt gaggatgata      360
38 ctagcatacc aactgatgaa aaggttccca tcctgatagc ttttcaccgg cacatatacg      420
39 atactgattg gcattattca tgtggtacga aggagtacaa gatttataatg gaccaatttc      480
40 accatgtttc tgcagctttt ttggaacttg aaaaagggtg tcaagaggct atcgaggaaa      540
41 ttactagaag aatgggtgca gggatggcca agtttatctg ccaagaggta gaaactgttg      600
42 atgactacga tgaatactgc cactatgttg ctgggcttgt tgggttaggt ttgtcgaaac      660
43 tcttcctcgc tgcaggatca gaggttttga caccagattg ggaggcgatt tccaattcaa      720
44 tgggttttatt tctacagaaa acaaacatta tcagagatta tcttgaggac attaatgaga      780
45 taccaaaatc ccgcatgttt tggcctcgcg agatttgggg caaatatgct gacaagcttg      840
46 aggatttaaa atacgaggag aacacaaaca aatccgtaca gtgcttaaat gaaatgggta      900
47 ccaatgcgtt gatgcatatt gaagattgcc tgaaatacat ggtttccttg cgtgatcctt      960
48 ccatatttcg gttctgtgcc atccctcaga tcatggcgat tggaacactt gcattatgct      1020
49 ataacaatga acaagtattc agaggcgttg tgaaactgag gcgaggctct actgctaaag      1080
50 tcattgatcg tacaaagaca atggctgatg tctatggtgc tttctatgat ttttctgca      1140
51 tgctgaagac aaaggttgac aagaacgacg caaatgccag taagacacta aaccgacttg      1200
52 aagccgttca gaaactctgc agagacgctg gagttcttca aaacagaaaa tcttatgtta      1260
53 atgacaaaagg acaaccaaac agtgtcttta ttataatggt tgtgattcta ctggccatag      1320

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54 tctttgcata tctcagagca aactgagtga tccatgtaag cgagtctgat tgtatcacca      1380
55 tcattcaaga tgttcagagc aaatttgagt gatgaagtaa tctaggttga ttcttattca      1440
56 cgccactgaa tcctaagcaa gattgtttcc agaacaaaca gagtttaagc atggttttagt      1500
57 ctaaaaccat ggattctatt ttagttacta ccttcgttgt ctaaactgtc atttgttcat      1560
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65 <400> SEQUENCE: 2
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68 Leu Leu Lys Met Lys Arg Ala Ile Glu Lys Ala Glu Lys Gln Ile Pro
69 20 25 30
70 Pro Glu Pro His Trp Gly Phe Cys Tyr Ser Met Leu His Lys Val Ser
71 35 40 45
72 Arg Ser Phe Ser Leu Val Ile Gln Gln Leu Asn Thr Glu Leu Arg Asn
73 50 55 60
74 Ala Val Cys Val Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
75 65 70 75 80
76 Asp Asp Thr Ser Ile Pro Thr Asp Glu Lys Val Pro Ile Leu Ile Ala
77 85 90 95
78 Phe His Arg His Ile Tyr Asp Thr Asp Trp His Tyr Ser Cys Gly Thr
79 100 105 110
80 Lys Glu Tyr Lys Ile Leu Met Asp Gln Phe His His Val Ser Ala Ala
81 115 120 125
82 Phe Leu Glu Leu Glu Lys Gly Tyr Gln Glu Ala Ile Glu Glu Ile Thr
83 130 135 140
84 Arg Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Gln Glu Val Glu
85 145 150 155 160
86 Thr Val Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val
87 165 170 175
88 Gly Leu Gly Leu Ser Lys Leu Phe Leu Ala Ala Gly Ser Glu Val Leu
89 180 185 190
90 Thr Pro Asp Trp Glu Ala Ile Ser Asn Ser Met Gly Leu Phe Leu Gln
91 195 200 205
92 Lys Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro
93 210 215 220
94 Lys Ser Arg Met Phe Trp Pro Arg Glu Ile Trp Gly Lys Tyr Ala Asp
95 225 230 235 240
96 Lys Leu Glu Asp Leu Lys Tyr Glu Glu Asn Thr Asn Lys Ser Val Gln
97 245 250 255
98 Cys Leu Asn Glu Met Val Thr Asn Ala Leu Met His Ile Glu Asp Cys
99 260 265 270
100 Leu Lys Tyr Met Val Ser Leu Arg Asp Pro Ser Ile Phe Arg Phe Cys
101 275 280 285
102 Ala Ile Pro Gln Ile Met Ala Ile Gly Thr Leu Ala Leu Cys Tyr Asn
103 290 295 300
104 Asn Glu Gln Val Phe Arg Gly Val Val Lys Leu Arg Arg Gly Leu Thr

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105 305          310          315          320
106 Ala Lys Val Ile Asp Arg Thr Lys Thr Met Ala Asp Val Tyr Gly Ala
107          325          330          335
108 Phe Tyr Asp Phe Ser Cys Met Leu Lys Thr Lys Val Asp Lys Asn Asp
109          340          345          350
110 Pro Asn Ala Ser Lys Thr Leu Asn Arg Leu Glu Ala Val Gln Lys Leu
111          355          360          365
112 Cys Arg Asp Ala Gly Val Leu Gln Asn Arg Lys Ser Tyr Val Asn Asp
113          370          375          380
114 Lys Gly Gln Pro Asn Ser Val Phe Ile Ile Met Val Val Ile Leu Leu
115 385          390          395          400
116 Ala Ile Val Phe Ala Tyr Leu Arg Ala Asn
117          405          410
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 69
121 <212> TYPE: DNA
122 <213> ORGANISM: Arabidopsis thaliana
124 <400> SEQUENCE: 3
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126 gcaaaactga                                     69
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129 <211> LENGTH: 22
130 <212> TYPE: PRT
131 <213> ORGANISM: Arabidopsis thaliana
133 <400> SEQUENCE: 4
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135 1          5          10          15
136 Ala Tyr Leu Arg Ala Asn
137          20
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140 <211> LENGTH: 1164
141 <212> TYPE: DNA
142 <213> ORGANISM: Arabidopsis thaliana
144 <400> SEQUENCE: 5
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146 aaacgagcga ttgagaaagc ggagaagcag atccctcctg agccacactg gggtttctgc      120
147 tattcgatgc tccacaaggt ttcccgaagc ttttctctcg ttattcagca actcaacacc      180
148 gagctccgta acgccgtgtg tgtgttctac ttggttctcc gagctcttga tactgttgag      240
149 gatgatacta gcataccaac tgatgaaaag gttcccatcc tgatagcttt tcaccggcac      300
150 atatacgata ctgattggca ttattcatgt ggtacgaagg agtacaagat tctaattggac      360
151 caatttcacc atgtttctgc agcttttttg gaactgaaa aagggtatca agaggctatc      420
152 gaggaaatta ctagaagaat ggggtgcagg atggccaagt ttatctgcca agaggtagaa      480
153 actgttgatg actacgatga aactgccac tatgttgctg ggcttggttg tttaggtttg      540
154 tcgaaactct tcctcgctgc aggatcagag gttttgacac cagattggga ggcgatttcc      600
155 aattcaatgg gtttatttct acagaaaaca aacattatca gagattatct tgaggacatt      660
156 aatgagatac caaaatcccg catgttttgg cctcgcgaga tttggggcaa atatgctgac      720
157 aagcttgagg atttaaaata cgaggagaac acaaacaaat ccgtacagtg cttaaatagaa      780
158 atggttacca atgcgttgat gcatattgaa gattgcctga aatacatggt ttccctgcgt      840
159 gatccttcca tatttcggtt ctgtgccatc cctcagatca tggcgattgg aacacttgca      900

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160 ttatgctata acaatgaaca agtattcaga ggcgttgga aactgaggcg aggtottact      960
161 gctaaagtca ttgatcgtaac aaagacaatg gctgatgtct atggtgcttt ctatgatttt      1020
162 tcctgcatgc tgaagacaaa gggtgacaag aacgatccaa atgccagtaa gacactaaac      1080
163 cgacttgaag ccgttcagaa actctgcaga gacgctggag ttcttcaaaa cagaaaatct      1140
164 tatgttaatg acaaaggaca acca                                           1164
166 <210> SEQ ID NO: 6
167 <211> LENGTH: 388
168 <212> TYPE: PRT
169 <213> ORGANISM: Arabidopsis thaliana
171 <400> SEQUENCE: 6
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173 1 5 10 15
174 Leu Leu Lys Met Lys Arg Ala Ile Glu Lys Ala Glu Lys Gln Ile Pro
175 20 25 30
176 Pro Glu Pro His Trp Gly Phe Cys Tyr Ser Met Leu His Lys Val Ser
177 35 40 45
178 Arg Ser Phe Ser Leu Val Ile Gln Gln Leu Asn Thr Glu Leu Arg Asn
179 50 55 60
180 Ala Val Cys Val Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr Val Glu
181 65 70 75 80
182 Asp Asp Thr Ser Ile Pro Thr Asp Glu Lys Val Pro Ile Leu Ile Ala
183 85 90 95
184 Phe His Arg His Ile Tyr Asp Thr Asp Trp His Tyr Ser Cys Gly Thr
185 100 105 110
186 Lys Glu Tyr Lys Ile Leu Met Asp Gln Phe His His Val Ser Ala Ala
187 115 120 125
188 Phe Leu Glu Leu Glu Lys Gly Tyr Gln Glu Ala Ile Glu Glu Ile Thr
189 130 135 140
190 Arg Arg Met Gly Ala Gly Met Ala Lys Phe Ile Cys Gln Glu Val Glu
191 145 150 155 160
192 Thr Val Asp Asp Tyr Asp Glu Tyr Cys His Tyr Val Ala Gly Leu Val
193 165 170 175
194 Gly Leu Gly Leu Ser Lys Leu Phe Leu Ala Ala Gly Ser Glu Val Leu
195 180 185 190
196 Thr Pro Asp Trp Glu Ala Ile Ser Asn Ser Met Gly Leu Phe Leu Gln
197 195 200 205
198 Lys Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Ile Asn Glu Ile Pro
199 210 215 220
200 Lys Ser Arg Met Phe Trp Pro Arg Glu Ile Trp Gly Lys Tyr Ala Asp
201 225 230 235 240
202 Lys Leu Glu Asp Leu Lys Tyr Glu Glu Asn Thr Asn Lys Ser Val Gln
203 245 250 255
204 Cys Leu Asn Glu Met Val Thr Asn Ala Leu Met His Ile Glu Asp Cys
205 260 265 270
206 Leu Lys Tyr Met Val Ser Leu Arg Asp Pro Ser Ile Phe Arg Phe Cys
207 275 280 285
208 Ala Ile Pro Gln Ile Met Ala Ile Gly Thr Leu Ala Leu Cys Tyr Asn
209 290 295 300
210 Asn Glu Gln Val Phe Arg Gly Val Val Lys Leu Arg Arg Gly Leu Thr

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211 305                      310                      315                      320
212 Ala Lys Val Ile Asp Arg Thr Lys Thr Met Ala Asp Val Tyr Gly Ala
213                      325                      330                      335
214 Phe Tyr Asp Phe Ser Cys Met Leu Lys Thr Lys Val Asp Lys Asn Asp
215                      340                      345                      350
216 Pro Asn Ala Ser Lys Thr Leu Asn Arg Leu Glu Ala Val Gln Lys Leu
217                      355                      360                      365
218 Cys Arg Asp Ala Gly Val Leu Gln Asn Arg Lys Ser Tyr Val Asn Asp
219                      370                      375                      380
220 Lys Gly Gln Pro
221 385
223 <210> SEQ ID NO: 7
224 <211> LENGTH: 31
225 <212> TYPE: DNA
226 <213> ORGANISM: Arabidopsis thaliana
228 <400> SEQUENCE: 7
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231 <210> SEQ ID NO: 8
232 <211> LENGTH: 28
233 <212> TYPE: DNA
234 <213> ORGANISM: Arabidopsis thaliana
236 <400> SEQUENCE: 8
237 cgggatccat ggggagcttg gggacgat                                     28
239 <210> SEQ ID NO: 9
240 <211> LENGTH: 31
241 <212> TYPE: DNA
242 <213> ORGANISM: Arabidopsis thaliana
244 <400> SEQUENCE: 9
245 ggaattctca tggttgtcct ttgtcattaa c                               31
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248 <211> LENGTH: 150
249 <212> TYPE: DNA
250 <213> ORGANISM: Arabidopsis thaliana
252 <400> SEQUENCE: 10
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255 gacgacaagg ccatggctga tatcggtacc                                     150
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258 <211> LENGTH: 50
259 <212> TYPE: PRT
260 <213> ORGANISM: Arabidopsis thaliana
262 <400> SEQUENCE: 11
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265 Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
266                      20                      25                      30
267 Ser Pro Asp Leu Gly Thr Asp Asp Asp Lys Ala Met Ala Asp Ile
268                      35                      40                      45
269 Gly Ser

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,130A

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TIME: 14:29:07

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03222002\J024130A.raw